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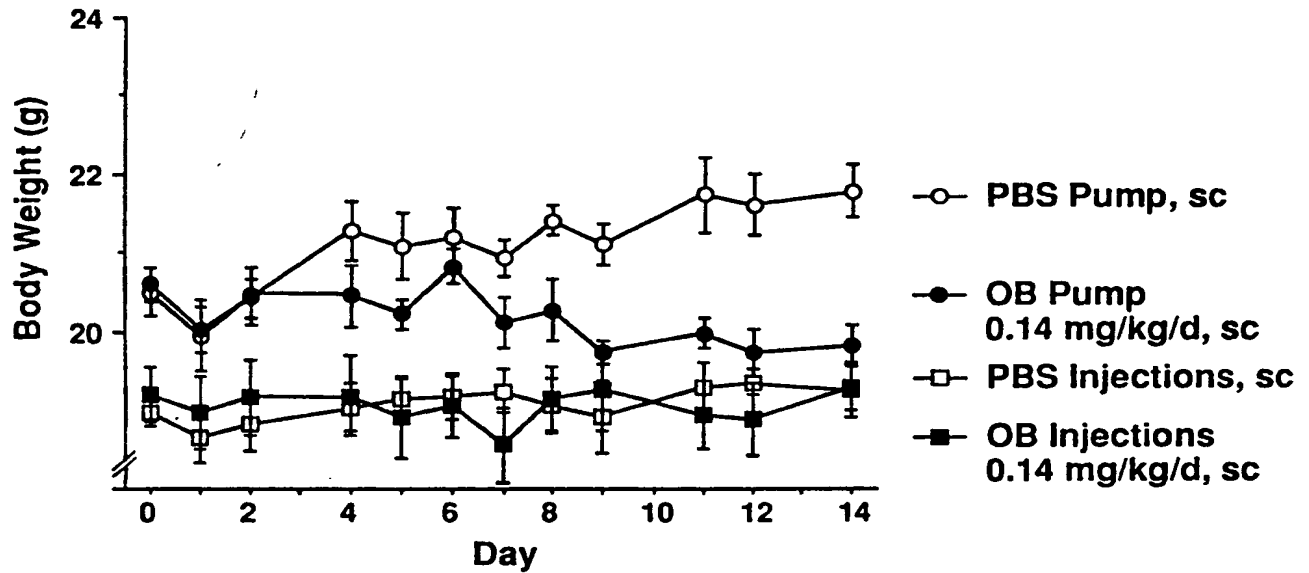


FIG. 1A

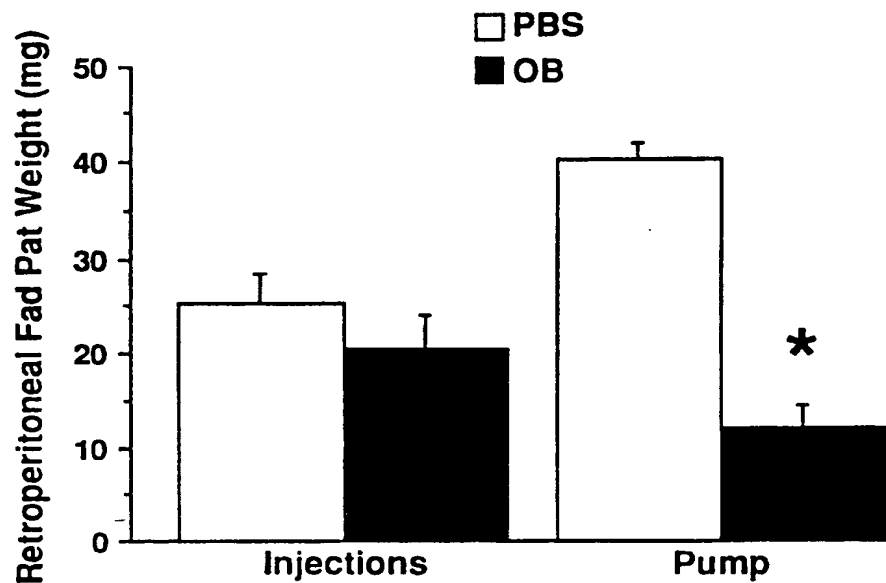


FIG. 1B

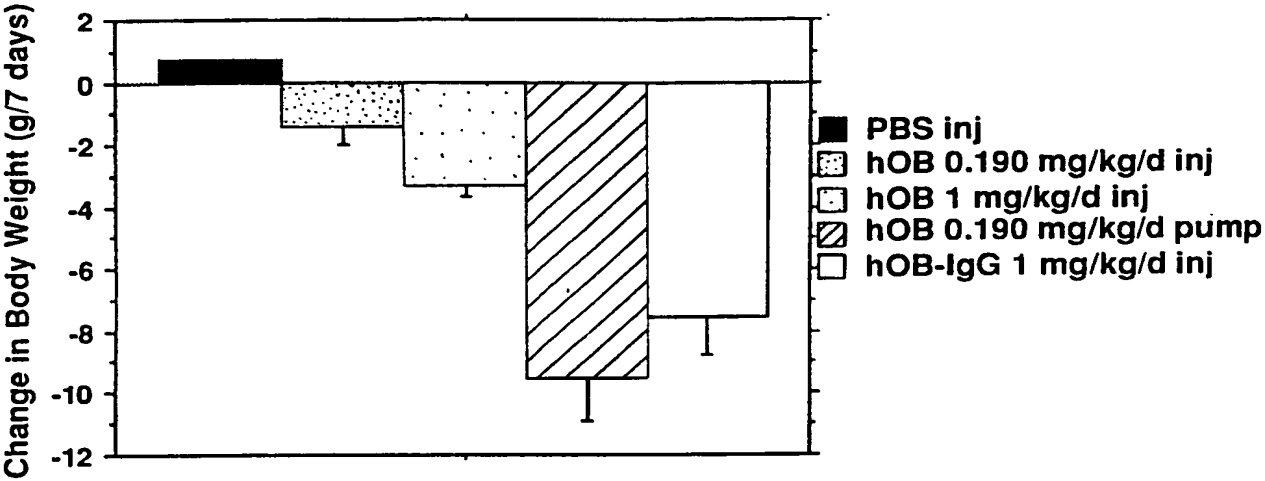


FIG. 2A

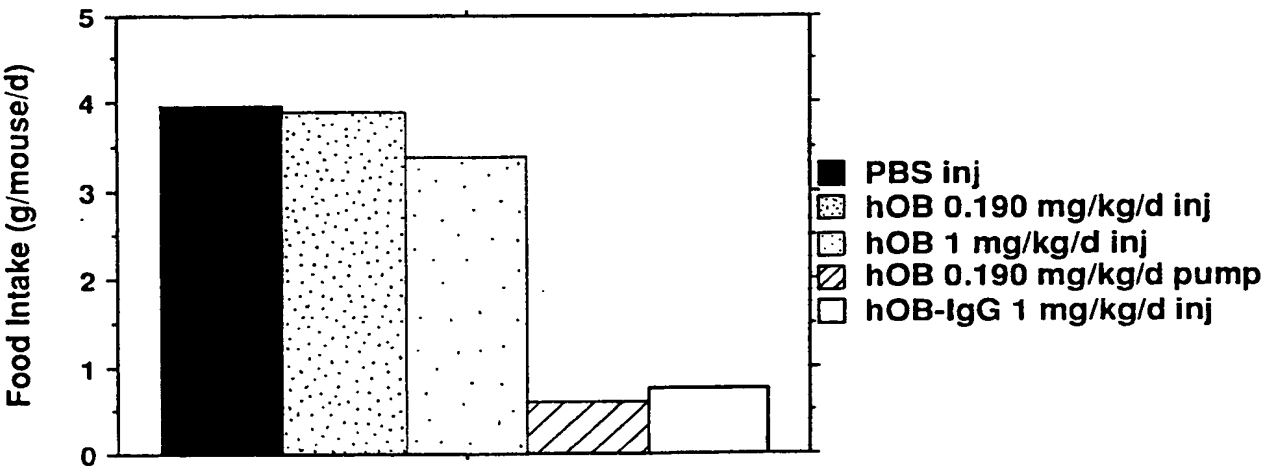


FIG. 2B

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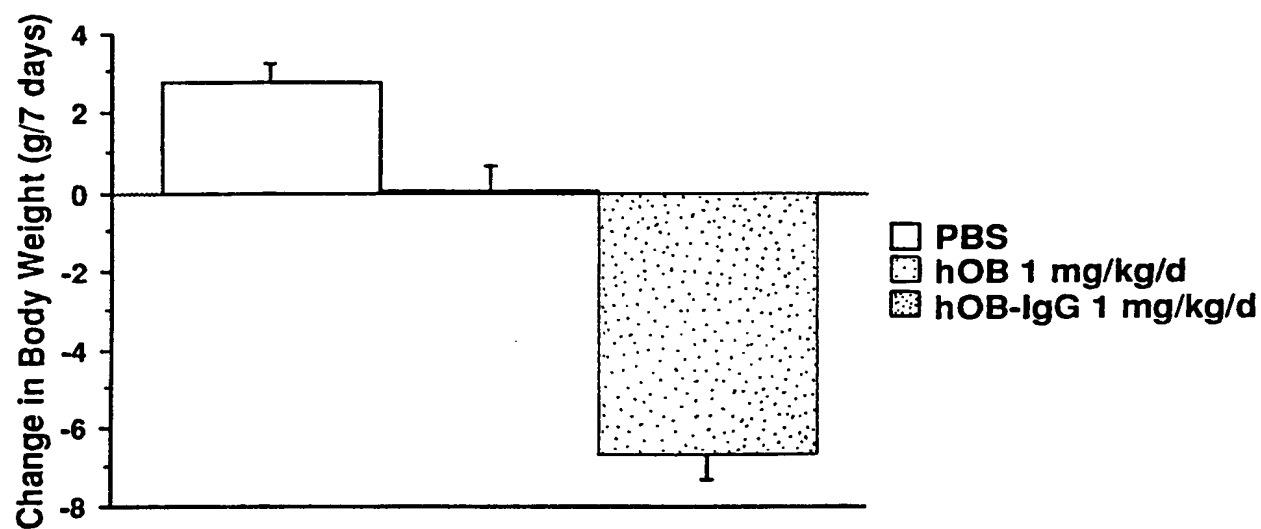


FIG. 3A

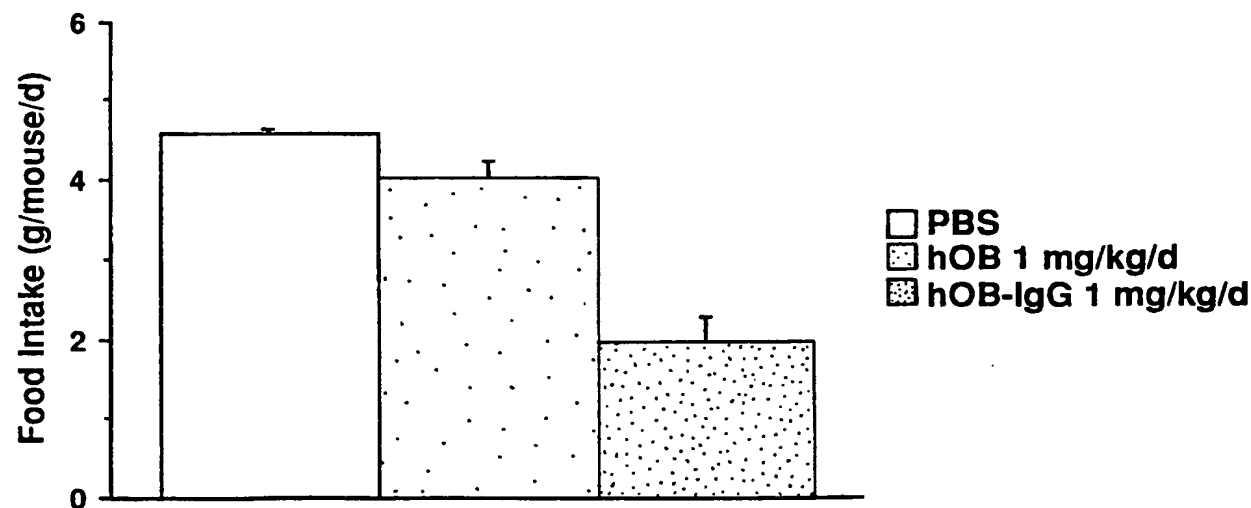


FIG. 3B

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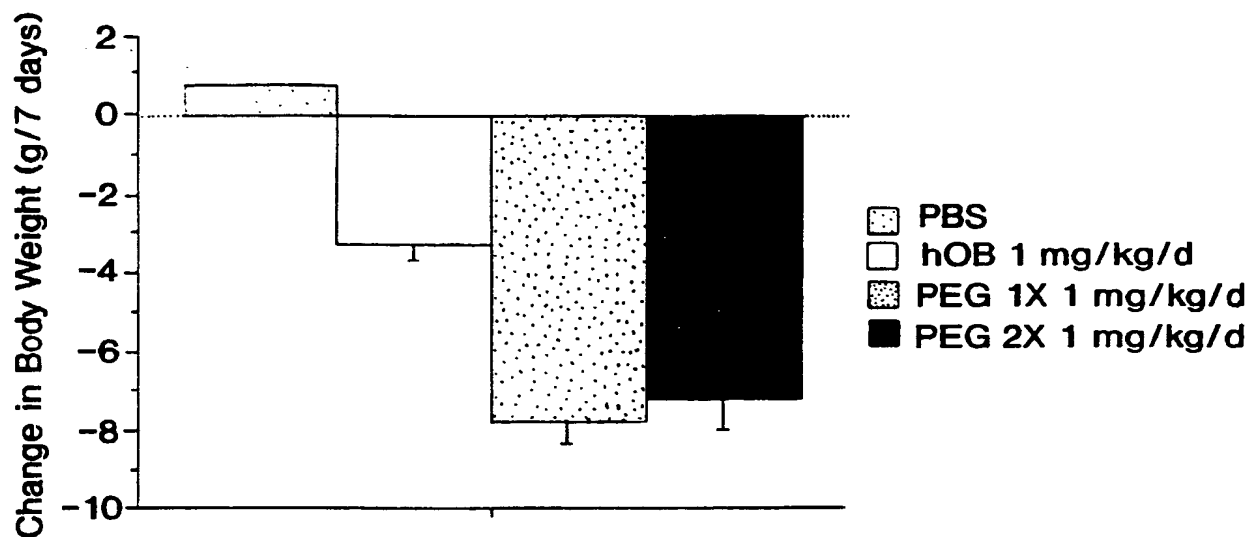


FIG. 4A

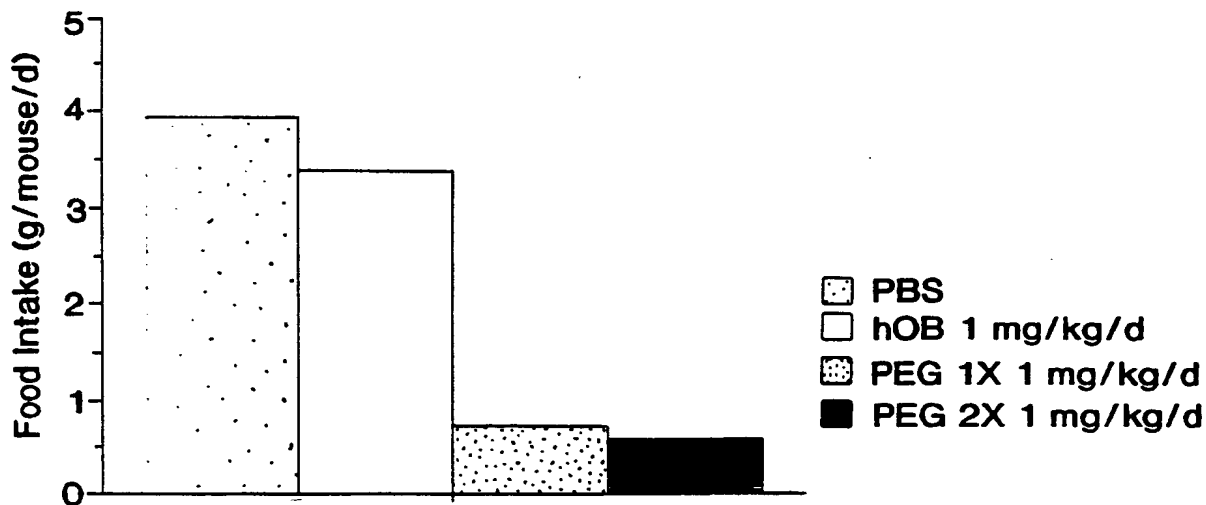


FIG. 4B

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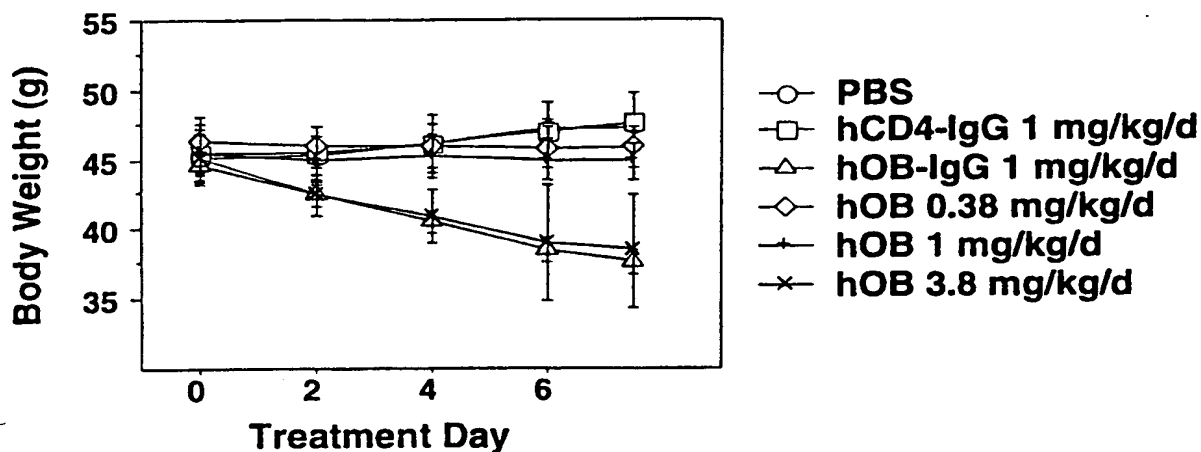


FIG. 5A

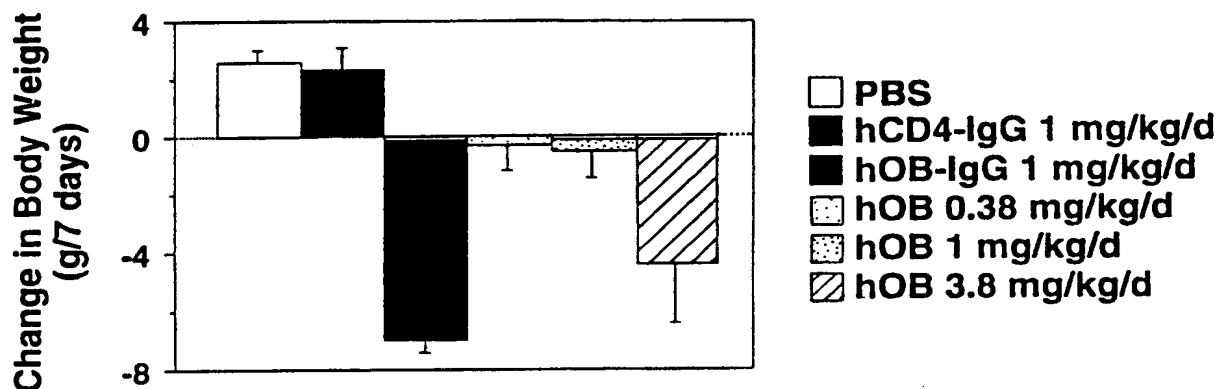


FIG. 5B

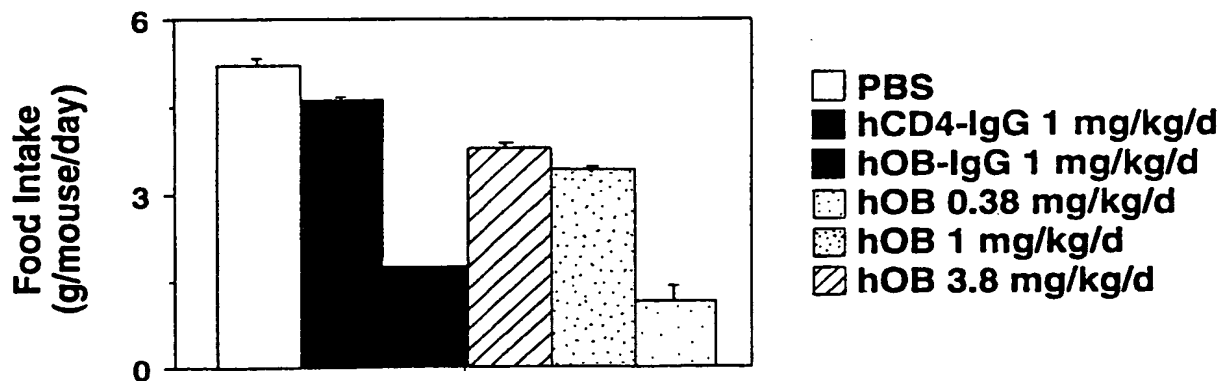


FIG. 5C

0
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8
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A
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C
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z
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haeIII/palI
mcrI
eagI/xmaIII/ecI XI
eaeI
cfrI
fnu4HI
aciI
thaI
fnuDII/mvni
sacII/satII
nap8II
kspI scrFI
dsal ncII
bglI bslI mspI
sau3AI mnlI bstUI
mboI/ndeII(dam-) hpaII
dplI(dam+) bsaJI dsav
dplI(dam-) bsh1236I
alwI(dam-) aciI cauII
fnu4HI
aciI
thaI
fnuDII/mvni tru9I
bstUI mseI
bsh1236I
aseI/asnI/vspI
bsh1236I
ggcTTCGT TA
gAACCGGCT ACAATTAA TA
CCTTGGCGCA TGTTAATTAT
~sp6 promoter

FIG. 6C

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26220*E9966/80

```

sau96I
avaII
asuI
scrFI
mvaI
ecorII
dsav
bstNI
apyl(dcm+)

maeIII
hphI scfI foki
balI bsajI
801 CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACAGGTGT CCACTCCCAG GTCCAACCTGC
GTATTGGAAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGGTGAAA CGGAAGAGAG GGTGTCCACA GGTGAGGTG CAGGTTCACG
*sp6 RNA start

ppu10I tfII sau96I
mnII taqI nsII/avaIII hinfI haeIII/palI bsp1286
bsaJI clai/bspl06 nlaIV acII asuI aluI bmyI foki
901 ACCTCGGTC TATCGATATG CATTCGGGAA CCCTGTGCGG ATCTTGTGG CTTTGGCCCT ATCTTTCTA TGTCCAAGCT GTGCCCCATCC AANAAGTCCA
TGGAGCCNAG ATAGCTATAC GTAACCCCTT GGGACACGCC TAAGAACACC GAAACCGGGA TAGAAAGAT ACAGGTTCGA CACGGGTAGG TTTTCAGGT
1 Met HistripGlyt hrLeuCysGI yPheLeuTrp LeuTrpProt yrLeuPheTy rValGlnAla ValProIleG InLysValGln
^cloning linker ^human OB start

sau3AI
mbol/ndeII(dam-)
dpmI(dam+)
scrFI
mvaI
ecorII
dsav
bstNI
apyl(dcm+)
hphI dpmII(dam-)
mnII muniI maeIII alvi(dam-) bsmAI
1001 AGATGACACC AANAACCTCA TCAAGACAAT TGTACACAGG ATCAATGACA TTTCACACAC GCAGTCAGTC TCCTCCAAAC AGAAGTCAC CGGTTTGGAC
TCTACTGTGG TTTTGGAGT AGTTCTGTTA ACAGTGGTCC TAGTTACTGT AAAGTGTGTG CGTCAGTCAG AGGAGTTTG TCTTCAGTG GCCAACCCTG
29 AspAspThr LysThrLeuI leLysThrII leLysThrArg IleAsnAspI leSerHisTh rGlnSerVal SerSerLysG InLysValTh rGlyLeuAsp

```

FIG. 6D

Quebec, 1990

FIG. 6E

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20230306280

```

scrFI      eam11051
mvaI       sau961
ecorII
dsav
bstNI
bslI
bsaJI      hphI      nlaIII      nspI      nspHI      bsp1286      bmyI alwNI
ddeI apyI{dcm+} maelII      nlaIII      nspI      nspHI      bsp1286      bmyI alwNI
mnlI bsaJI aciI bstEII      nlaIII      nspI      nspHI      bsp1286      bmyI alwNI
1401 GACCTCAGCC CTGGGTGCGG GGTACCCGAC AAAACTCACA CATGCCACACC GTGCCGAGCA CCTGAACCTCC TGGGGGACC GTGAGTCTTC CTCTTCCCCC
CTGGAGTCGG GACCCACGCC CCAGTGGCTG TTTTGAGTGT GTACGGGTGG CACGGGTGCT GGACTTGAGG ACCCCCTGG CAGTCAGAG GAGAGGGGGG
162 AspleuSerp roGlyCysG1 yValThrAsp LysThrHisT hrCysProPr oCysProAla ProGluLeuL euGlyGlyPr oSerValPhe LeuPheProPro
^Insertion of a gly
^START OF HUMAN IgG1 CH2CH3

sau96I
nlaIV
mspI
hpall
scrFI
ncil
dsav
sauJAI      avall
mboI/ndeII{dam-}      nlaIII
nlaIII      caulI      mnlI      nspI
rcal dplI{dam+}      ddel      nspHI
bspHI{dam-}      asuI eco8II maelII
styl      mnlI      dplII{dam-}      bsu36I/mstII/sauI
bsaJI      CAAACCCCA GGACACCTC ATGATCTCC GGACCCCTGA GGTACATGC GTGGTGGTGG ACCTGAGCCA CGAGACCTT GAGGTCAAGT TCAACTGGTA
GTTTGGGT CCTGTGGAG TACTAGAGG CTGGGGGACT CCAGTGTACG CACCACACC TGCACCTCGT GCTTCTGGGA CTCAGTTCA AGTTGACCAT
196 LysProLy sasPThrLeu MetIleSera rgThrProG1 uValThrCys ValValVala spValSerHI sGluAspPro GluValLysP heAsnTrpTyr

```

FIG. 6F

[illegible][illegible]

FIG. 6G

2022030906280

mspI
hpaiI
fnu4HI
bbvI

pleI
hinfI
mnII
nlaIV mboII scfI
alul bsaJI

dsai
hphI
alul bsaJI

201 CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACCTAC AAGACCACGC CTCCCGTGCT GGACTCCGAC GGTCTCTTCT TCCTCTACAG CAAGCTCACC
GCACCTCACC CTCTCGTTAC CCGTGGGCTT CTGTGTGATG TTCTGTGCG GAGGCCACGA CCTGAGGCTG CCGAGGAGA AGGAGATGTC GTTCGAGTGG
329 ValGluTrp GluSerAsnG lyGlnProG uasAsnTyr LysThrThrP roProValle uasPserAsp GlySerPheP heLeuTyrSe rLysLeuThr

bspMI bbvI
fnu4HI xmnI bbsI
asp700 nlaIII
sfaNI mnII

ppu10I
nsII/avaIII

scrFI
ncII
mspI
hpaiI
dsav

2001 GTGCACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT GCTCCGTGAT GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC TCCCTGTCTC
CACCTGTTCT CTGCCACCGT CGTCCCTTG CAGAAGAGTA CGAGGCACTA CGTACTCCGA GACGTGTTGG TGATGTGGT CTTCCTGGAG AGGCACACAG
362 ValaspLysS erArgTrpG1 nGlnGlyAsn ValPheSerC ysSerValme tHisGluAla LeuHisAsnH lstyThrG1 nLysSerLeu SerLeuSerPro

taqI
sali
pleI scfI
rmaI hincII/hindII
sau96I hinfI pstI
haeIII/palI bsgI
asuI maeI accI bspMI hindIII hinfI bspHI hindIII acII asuI

alul
fnu4HI
bbvI

maeIII
sfanI apol

rmal
bsmI maeI

2201 TATAATGTT ACAATAAAG CAATACCATC ACAATTTC CAAATAAAGC ATTTTTTCA CTGCATTCTA GTTGCTGTTT GTCCAAACTC ATCAATGTAT
ATATTACCAA TGTTTATTTC GTTATCGTAG TGTTTAAAGT GTTTATTTCG TAAAAAAGT GACGTAAAGT CAACACCAA CAGGTTTGAG TAGTTACATA

2101 CGGGTAAATG AGTCCGACGG CCTTAGAGTC GACCTGCAGA AGCTTCTAGA GTCGACCTGC AGAAGCTTGG CCGCCATGGC CCAACTTGTT TATTGCAGCT
GCCCATTTAC TCAGGCTGCC GGGATCTCAG CTGCAGCTCT TCGAAGATCT CAGCTGCAGG TCTTCGAACC GCGGTACCG GGTGGAACAA ATACGTCGA
396 GlyLys

^sv40 early poly A

FIG. 6H

Abstract

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[illegible]

FIG. 61

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26220 2996280

```

fnu4HI
bglI
sfII
haeIII/palI
mnlI mnlI ddeI
haeIII/palI bsaJI mnlI aluI
mnlI bsaJI acII haeIII/palI
mnlI bsaJI acII AGGCCGAGC CGCCTCGCC TCTGAGCTAT
CGGCCGCTAA CTCGCCCAT TCCGCCCAT ATGCTGACT AATTTTTTTT ATTATCCAG AGGCCGAGC CGCCTCGCC TCTGAGCTAT
CGGCCGCTAT GAGCGGGTC AAGCGGGTA AGAGCGGGT TACCCTGTA TAAAAAAA TAAATAGCTC TCCGCTCCG CGCGAGCGG AGACTCGATA

```

```

scfI
mvaI
sau96I
nlaIV
avaII sau96I
thaI ecorII
fnuDII/mvnl
bstUI dsav
bsh1236I avaII
hinPI bstNI
hhai/cfoI asuI
fnu4HI asuI apyI(dcm+)
acII acII bsaJI
sfuI
bstBI
bsiCI
asuII
tru9I
alul msel taqI sfaNI
TTGCAAAAG CTGTTAATC GAACACGAG ATGAGTCGG CGCGGGCGG TCCAGSTCC
AGCTCTTCAT CACTCTCTCG AAAAACCTC CGATCCGAA AACTTTTTT GACATTAAG CTGTGCTC TACGTCAGC CGCGGGCGG AGGTCCAGG
*start pUC118

```

~TK promoter

```

sau3AI
mboI/ndeII(dam-)
dpnI(dam+)
sau3AI
mboI/ndeII(dam-)
dpnI(dam+)
bstYI/xhoII
bglII dpnII(dam-)
tru9I hincII/hindII acII dpnII(dam-) bsmAI
acII msel hgaI fnu4HI bclII(dam-)
TCAACACCG CTTAACACCG TCAACACCGT CGCCGAGATC TGATCAAGAG
GATTGTGCG GATTGTGCG GATTGTGCG GATTGTGCG GATTGTGCG GATTGTGCG GATTGTGCG GATTGTGCG GATTGTGCG GATTGTGCG
tn5 neomycin phosphotransferase gene.

```

FIG. 6J

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26220 2336280

```

sau3AI
mboI/ndeII{dam-}
dpmI{dam+}
dpmII{dam-}
mnlI
mamI{dam-}
bsaBI{dam-}
fokI alvi{dam-} nlaIII
2901 ACAGGATGAG GATCGTTTCG CATGATTGAA CAAGATCGAT TGCACGCAGG TTCTCCGCC GCTTGGTGG AGAGCTATT CGGCTATGAC TGGGCACAAC
TGTCTACTC CTAGCAAGC GTACTAATT GTTCTACTTA AGTGGGTCC AAGAGGCCG CGAACCCACC TCTCCGATAA GCCGATACG ACCCGTGTG

acII
fnu4HI
haeIII/palI
mcrI
eagI/xmaIII/ecI XI
eaeI
cfrI
mspI
hpaII
bspHI
hpaII
mnII
bsrI
bsp1286
bmyI

hlnPI
hhaI/cfoI
nlaIV
nari scrFI
kasi nciI
hinII/acyI
hgiCI mspI
haeII hpaII
bani dsav
hinPI ahaII/bsaHI
hhaI/cfoI cauli
3001 AGACAATCGG CTGCTCTGAT GCCGCCGTGT TCCGGCTGTC AGCCGAGGG CGCCCGTTC TTTTGTCAA GACCGACCTG TCCGCTGCC TGAATGAAT
TCTGTAGCC GACGAGACTA CGCGGCACA AGCCGACAG TCCGCTCCC CGCGGCCAAG AAAACACTT CTGCTGGAC AGCCACGGG ACTTACTTGA

acII
fnu4HI
bsaNI bslI
bbvI
3101 GCAGGACGAG GCAGCGCGG TATCGTGGCT GGCACGACG GCGTTCCTT CGCGAGGAA CGCGTGTGC CGCAACCGA CCGTGTGCTC ATAGCACCGA
CGTCTGCTC CGTGGCGCG ATAGCACCGA CCGTGTGCTC CGCGTGTGCA CAGTGACTTC GCCCTTCCCT GACCGACGAT

hgiAI/aspHI
bsp1286
alul
pvuII
fnu4HI
bbvI bslHKAI
hinPI bmyI
hhaI/cfoI
mstI nspBII
avIII/fspI
taqI
maeIII acII
fnu4HI
bsrI bbvI

```

FIG. 6K

[illegible]

FIG. 6L

FIG. 6M

[illegible][illegible]

FIG. 6N

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[illegible]

FIG. 60

08/793653
PCT/US96/20718

4401 GCCGCCGGAC GAACATAACC ATCTCTCGCC CTCTCTCGCT GGTACGAGGA GCGCTTTTGT TTTGTATTGG TCACCACGGC CGAGTTTCCG
 bslI sfanI mboII csp6I eco47III
 mspI hlnPI
 hpalI mnII hhaI/cfoI
 acII rsaI haeII
 fnu4HI
 mcrI
 haeIII/palI bsh1236I
 sacII/sstII
 bstOI
 fnuDII/mvni
 thal
 acII

bsaJI bstNI
 sau96I bsaJI
 nlaIV haeIII/paII
 avall eaeI
 asuI cfrI bsp1286
 ppuHI mspI apyI[dcM+]
 nlaIV hpaII bmyI
 ecoO109I/draII bani
 4501 CGGGACCCG GCCAGGCAC CTGTCTACG AGTTGCATGA TAAAGAGAC AGTCATAAGT GCGCGCAGCA TAGTCATGCC CCGCGCCAC CGGAAGGAGC
 GCCTTGGGC CGGTCCGTG GACAGGATGC TCAACGTACT ATTTCTTCTG TCAGTATTCA CCGCGCTGCT ATCAGTACGG GCGCGGGTG GCCTTCCTCG
 ^pBR322 sequence

FIG. 6P

[illegible][illegible]

FIG. 6Q

[illegible]

thaI
fnuDII/mvnl
tru9I apoI tru9I
mseI bstUI mseI
tru9I mseI
apoI bsh1236I
sapI
5001 GGGCTATTCT TTGATTAT AAGGATTTT GCCGATTTCG GCCTATTGCT TAAAAATGA GCTGATTATA CAAAAATTA ACAGCAATTT TAACAAATA
CCCGATAAGA AACTAATA TTCCCTAANA CGGCTAAGC CGGATAACCA ATTTTITACT CGACTAAAT GTTTTAAAT TGCCTTAA ATTGTTTAT
maeII
psp1406I
tru9I
mseI
mnII
haeIII/palI
stui
haeI
maeII
hlnII/acyI
ahaII/bsaHI
nlaIII
tru9I rcaI
mseI bspHI
ddei aatII
5101 TTAACGTTTA CAATTTATG GTGCAGGCT CGTGATACGC CTATTTTAT AGTTTATGT CATGATAATA ATGTTTCTT AGAGTCAGG TGGCACTTTT
AATTGCAAT GTTAAATAC CAGTCCGA GCACATGCG GATAAATA TCCAATTACA GTACTATTAT TACCAAGAA TCTCAGTCC ACCGTGAAAA
~delta 2a
nlaIV
aciI
thaI
fnuDII/mvnl
bstUI
bsh1236I
hlnPI
hhai/cfoI
5201 CGGGGAATG TCGCGGGAAC CCTATTGT TTATTTTCT AATACATTC AATATGTAT CCGCTCATGA GACAATAACC CTGATAATG CTTCAAATAT
GCCCTTTAC ACGCGCTTG GGGATNACA ANTAANAAGA TTATGTAG TTTATACATA GCGAGTACT CTGTTATTGG GACTATTAC GAAGTTATTA
mboII
earI/bsp632I
5301 ATTGAAAAG GAAGAGTATG AGTATTCAAC ATTTCCCTGT CGCCCTTATT CCTTTTTTG CGGCATTTTG CCTTCCTGT TTTGCTCACC CAGAAACGCT
TAACTTTTC CTCTCATAC TCATAGTTG TAAAGGACA GCGGAATAA GCGGAATAA GCGGAATAA GCGGAATAA GCGGAATAA GCGGAATAA GCGGAATAA GCGGAATAA
hglAI/aspHI
bsp1286
sau3AI
mboI/ndeII[dam-]
dpmI[dam+] bmyI
dpmII[dam-]
eco57I
apaLI/snoI
alw4I/snoI
maeIII taqI alwI[dam-] aciI bstYI/xhoII
hphI
sfanI mboII[dam-]
5401 GGTGAAAGTA AAGATGCTG AAGATCAGTT GGTGTCACGA GTGGGTTACA TCGAAGTACA TCTCAACAGC GGTAAGATCC TTGAGAGTTT TCGCCCCGAA
CCACTTTTCA TTTCTAGCAC TTCTAGTCAA CCCACGTGCT CACCCAATGT ACCTTGACCT AGAGTTGTCT CCATCTAGG AACTCTCAA AGCGGGGCTT
mboII

FIG. 6R

[illegible]

FIG. 6T

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mspI
hpaII
bsaI
fnu4HI
bsaHI
acII

hpaI
hhaI/cfoI
haeII

acII

6701 CGAAGGACCT ACACCGAAGT GAGATACCTA CAGCGTGAGC ATTGAGAAG CGCAGCGCTT CCGGAAGGCA GAAAGCGGCA CAGGTATCCG GTAAGCGGCA GCTTGCTGGA TGTGCTTGA CTCTATGGAT GTGCACTCG TAACTCTTC GCGTGCGAA GGGCTTCCCT CTTTCCGCT GTCCATAGGC CATTCGCGCT

scrFI
mvaI
ecorII
dsaV
bstNI
bsaJI

scrFI
mvaI
ecorII
dsaV
bstNI
bsaJI

apyl[dcmt]
apyl[dcmt]

6801 GGGTCGGAC AGGAGAGGC ACGAGGAGC TTCCAGGGG AAGCGCTGG TATCTTTATA GTCTGTGCG GTTTCGCCAC CTCGACTTG ACGTGGATT CCCAGCCTG TCCTCTCGG TGTCTCCG AAGTCCCC TTTCCGACC ATAGAATAT CAGGACAGC CAAGCGGTG GAGACTGAC TCGACGTAA

alul
pvuII
nspBII

alul
pvuII
nspBII

bsrI
acII
acII
aseI/asnI/vspI

6901 TTTGTGATG TCGTCAGGG GCGGAGCCT ATGGAAAAC GCCAGTGGC ACGACAGGT TCCGACTGG AAGCGGCA GTGAGCGCA GCGAATTAA AAACACTAGC AGCAGTCCC CGGCTCGGA TACCTTTTG CGGTCGACC TCGTGTCCA AGGCTGACC TTTCCGCTT CACTCGCTT GCGTTAATTA

scrFI
mvaI
ecorII
dsaV

scrFI
mvaI
ecorII
dsaV

apyl[dcmt]
apyl[dcmt]

7001 GTGAGTTACC TCACTCATT GGCACCCAG GCTTACACT TTATGCTTC GGTCTGTATG TTGTGTGGA TTGTAGCGG ATACAAATT CACACAGGAA CACTCAATGG AGTGAGTAAT CCGTGGGTC CGAATGTGA AATACGAAG CCGAGCATAC AACACACCTT AACACTGCC TATGTATAA GTGTGTCTT

alul
nlaI
asp700

alul
nlaI
asp700

asp700

7101 ACAGCTATGA CCATGATTAC GAATTAA TGTGATACT GGTACTATG CTTAATT

FIG. 6V

>length: 7127

aatII(GACGTC): 150 203 286 472 5182